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.... Sandahan

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ProValSerGlyPheValAlaProHisGlnTyrLeuSerLeuGlnAs 175
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      gb_est40:AV697597
gb_est15:A1036595
gb_est39:AV620688
gb_est53:AW941467
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JOURNAL
COMMENT
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1 ALS84678 ALS84678 Stratagene CI

1 AA968411 uc71b05.y1 Sugano mous

AV550135 AV650135 GLC Homo sapi

1 C93903 C93903 Dictyostellum d1s

1 AA59643 um56c12.r1 Stratagene

AV65048 AV650368 CLC Homo sapi

1 AV65124 AV651521 GLC Homo sapi

1 AV65124 AV651521 GLC Homo sapi

AV65124 AV65158 GLC Homo sapi

AV65128 AV652188 GLC Homo sapi

AV652188 GLC Homo sapi

AV65148 AV652188 GLC Homo sapi

AV650405 LMAFYLL INGL GGAP

AA880857 vx46f08.r1 Stratagene

AQ902002 LMAFYLL IM94b04 x1 Lei

AU038515 AU038515 Dictyostellum

AV650433 AV650433 GLC Homo sapi

AU038515 AU038515 Dictyostellum

AV650433 GLC Homo sapi

AV650433 GLC Homo sapi
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AA685049 EST106124 Rat PC-12 ce
AV648130 AV648130 GLC Homo sapi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA913604 0138b10.sl Soares_NFL
BG563015 602581192F1 NIH_MGC_76
AL524765 AL524765 LTI_NFL003_NB
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AV655322 AV655322 GLC Homo sap
AV682023 AV682023 GKB Homo sap
                                                                                                                 Command line parameters:
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-GGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.000 -GGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -FGAPOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -FGAPOP=6.000
-LIST-45 -DOCALIGN=200 -THR_SCORE-PCT -TRANS=human40.cdi
-LIST-45 -DOCALIGN=200 -THR_SCORE-PCT -TRANS=human40.cdi
-LIST-45 -MODE-LOCAL -OUTFMT-PfS -NORM-ext -MINLEN=0
-MAXEN=200000000 -USER-US09438185_GGGN1_1_3303 -NCPU-6
                                                                   About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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OM of: US-09-438-185-1047 to: EST:*
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v 108-09-438-185-1047

Oi 1-1 length: 362

Datudase: EST:*
Database sequences: 10228115

Database length: 431459454

Search time (sec): 1175.810000
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gb_est4(1:AA568411

gb_est4(1:AA568411

gb_est103:AA568413

gb_est103:C33147

gb_est103:C33147

gb_est103:C33147

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gb_est103:AA586855

gb_est103:AA586857

gb_est103:AA682455

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gb_est103:AA68243340

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gb_est103:AA653322

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gb_est28:AL524765
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AV697597 AV697597 GKC HOMO S
AF1036595 LUG89411.91 SUGano m
AV620688 Chlamydomo
AW941467 HLO8079.3prime HL D
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Hybasianinae; Gallus.
I (bases 1 to 660)
Murray.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL584678 660 bp mRNA EST 28-FEB-2001
AL584678 Stratagene Chick Embryo Lambda cbNA Library (* 937405)
Gallus gallus cbNA clone ROS013B04; mRNA sequence.
AL584678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 ..GlnAlaValIleLySPhePheGluLeuGluThrHisPheSerTyrTyr 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCAGTAAACTCTATCCCACCCACGCTTGTCGTGAATATTTAAAAACTT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strategene Chick Embryo Lambda cDNA Library Unpublished (2001)
Contact: Frazer Murray Dept. Genomics and Bioinformatics Roslin Institute
Roslin, Mallothhan, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray&bbsrc.ac.uk
Seq primer: T3.
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Gaps: 3
Percent Identity: 28.182
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 669)

Marra, M. HillieriL., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelsing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA968411 669 bp mRNA EST 20-MAY-1998
C121b95.y1 Sugano mouse liver mia Mus musculus cDNA clone
IMAGE:1431057 5' similar to gb:K03020 PHENYLALANINE-4-HYDROXYLASE
(HUMAN); gb:X51942 Mouse mRNA for phenylalanine hydroxylase (MOUSE), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washugton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 snValArgValLeuProLeuGluLeuAspGlnIleIleArgLeuProPhe 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 yalaValLeuIleSerSerProGlnGluLeuGlyHisAlaPheIleAspA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :::::::|||
544 AGGCCAAGGTGAAAACATTCGATCCGAAGACAACCTGTTTGCAAGAATGC 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        594 CTTATCACCACTTTCAGGAAGCTTACTTTGTTTCAGAAAGTTNTGAAGA 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 AsnThrSerThrProGlnGluThrLeuPheSerIleArgHisPheAspGl 325
                                                                                                                                                                                                                                                                                                                                                                          225 eThrLysValIleGluLysValGlnAlaLeuProSerLysLysGlnArgI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 leGlnThrLeuGlnSerAsnLeuIleAlaIleValArgCysPheTrpPhe 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 TICAGAAATTAGCCACT .....TGCTATTTTT 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 ThrValGluSerGlyLeuIleGluAsnHisGluGlyArgLysAlaTyrGl 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    444 ACGATTGAATTTGGTCTTTGCAAGCAAGAAGGACAGCTACGTGCTTATGG 493
                                                                                                                                                                                                    292 ACACCCCAGAACCGGATACATGCCATGAACTTTTGGGACATGTGCCTCTA 341
                                                                                                                                                                                                                                                                           209 LeuLeuHisProSerPheSerGluPhePheIleAsnMetGlyArgLeuPh 225
                                                                                                                                                                                                                                                                                                                                                                                                                 192 CCGGTTGCTGGATATCTCTCCCCCGAGACTTTTTAGCTGGCTTAGCATA 241
                                                                       175 pargTyrPheProllealaSerValMetArgThrLeuAspLysAspAsnP 192
                                                                                                                                                                                                                                                                                                      242 CAGAGITITICACIGIACICAGIAIGIACGACACGGCICGGAICCICIT
                                                                                                                                                                            192 heSerLeuThrProAspLeuIleHisAspLeuLeuGlyHisValProTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouseest@watson.wustl.edu
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VERSION
KEYWORDS
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ORGANISM
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COMMENT
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                      384
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was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTT]; double stranded CDNA was ligated to a Draili adaptor [FOTTGGCCTACTGG], digested and cloned into distinct Draili sites of the pME18S-FL3 vector (5' site CACTGTGG, 3' site CACCATGTG; xhoI should be used to isolate the CDNA insert. Size selection was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTAAAAGCTGCG and 3' end primer CAACCTGCAGCACAA."
                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: liver; Vector: DME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:915125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 PheSerGluPhePheIleAsnMetGlyArgLeuPheThrLysValIleGl 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 ValAlaProHisGlnTyrLeuSerLeuLeuGlnAspArgTyrPheProIl 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 eAlaSerValMetArgThrLeuAspLysAspAsnPheSerLeuThrProA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 CACACAGTACATTAGGCATGGATCTAAGCCCATGTACACACCTGAACCTG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 spLeulleHisAspLeuLeuGlyHisValProTrpLeuLeuHisProSer 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 ATATCTGTCATGAACTCTTGGGACATGTGCCCTTGTTTCAGATAGAAGC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 uLysValGlnAlaLeuProSerLysLysGlnArglleGlnThrLeuGlnS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 AGTITCIGCAGACITGIACIGGITICCGCCICCGICCIGITGCIGGCITA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 PheSerLeuTrpLysSerTyrCysProArgPhePheLeuAspTyrLeuGl 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 uAlaPheGlyLeuLeuSerAspPheLeuAspHis...GlnAlaValIleL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 ysPhePheGluLeuGluThrHisPheSerTyrTyrProValSerGlyPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 .......GGTTTCCGTGAAGACAACATCCCGCAGCTGGAAGATGTTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 TTCCCTCTTCTGGAAAGTACTGC........
                                                                                                                                                                                                                                                                                                     /clone_lib="Sugano mouse liver mlia"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 4
Percent Identity: 30.688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 669
                                                                                                        Seq primer: primer name ambiguous
High quality sequence stop: 465.
Location/Qualiflers
                                                                                                                                                                                                           /organism="Mus musculus"/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1431057"
                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AA968411 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-438-185-1047 x AA968411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211.00
1.936
57.672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                        FEATURES
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Service of State Separate

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rTyrCysProArgPhePheLeuAspTyrLeuGluAlaPheGlyLeuLeuS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Dictyostelium discoideum"
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VERSION
KETWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                       162
120
                                                                                                          125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              406
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                                                                     137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota, Martazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Eukaryota, Martazoa, Chordata; Craniata; Hominidae; Homo.

1 (bases I to 607)
Olan, B., Wu, T., Huang, Q., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H.,
Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Qu, J.,
Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu
Homo sapiens cpn, clone
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Zeguang Han
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
1201203, P. R. China
1201203, P. R. China
Fax: 86-21-50801912[ex.45]
Fax: 86-21-50801922
Email: hanzgechgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="corresponding non cancerous liver tissue"/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                          AV650135 607 bp mRNA EST 07-SEP-2000 AV650135 GLC Homo sapiens cDNA clone GLCCBF06 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 ArgAsnLeuTrpTyrArgLeuLeuSerSerArgPheSerLeuTrpLysSe 120
                                                                                       264 LeuileGluAsnHisGluGlyArgLysAlaTyrGlyAlaValLeuileSe 280
                                                                                                               280 rSerProGlnGluLeuGlyHisAlaPheIleAspAsnValArgValLeuP 297
                                                                                                                                                                                    34 AAGAAAACATGGGGCACAGTGTTCAAGACTCTGAAGTCCTTGTATAAAAC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 others
                   247 erAsnLeuIleAlaIleValArgCysPheTrpPheThrValGluSerGly
                                       ..ATTTACTGGTTTACTGTGAGTTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 4
Percent Identity: 28.502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCCBF06"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AV650135 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 c
                                                                                                                                                                                                                                       297 roLeuGluLeuAspGln 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-438-185-1047 x AV650135
                                                                                                                                                                                                                                                               485 CCCTGGAGCTAGAGAG 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210.50
1.784
57.005
                                                                                                                                                                                                                                                                                                                   seq_name: qb_est40:AV650135
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
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AL SION
VERSION
KEYWORDS
SOURCE
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
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JOURNAL
COMMENT
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DEFINITION C93903 729 bp mRNA EST 08-JUN-1998 OBFINITION C93903 Dictyostellum discoideum SS (M.Yoshida) Dictyostellum discoideum cDNA clone SSL848, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Developmental cDNA in Dictyostellum discoideum (M.Yoshida) pubblished (1998)
Contact: Motonobu Yoshida
Research Institute of Food Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyostelium discoideum.

Dictyostelium discoideum

Dictyostelium discoideum

Licharyota; Mycetcoza; Dictyosteliida; Dictyostelium.

1 (Dases 1 to 729)

Yoshida,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 CCATGCT.....TGCTATGAGTACAATCACATTTTCCACTTCTTG 124
                                                                                                                 AAAAGTACTGTGGCTTCCATGAAGATAACATTCCCCAGCTGGAAGACGTT 174
                                                                                                                                                                           146 IleLysPhePheGluLeuGluThrHisPheSerTyrTyrProValSerGl 162
                                                                                                                                                                                                             175 TCTCAGTTCCTGCAGACTTGCACTGGTTTCCGCCTCCGACCTGTAGCTGG 224
                                                                                                                                                                                                                                                                                                                              225 CCTGCTTTCCTCTCGGGATTCTTGGGTGGCCTGGCCTTCCGAGTCTTCC 274
                                                                                                                                                                                                                                                                                                                                                                                                                 179 rolleAlaSerValMetArgThrLeuAspLysAspAsnPheSerLeuThr 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 ACTGCACAGTACATCAGACGATGGATCCAAGCCCATGTATACCCCCGAA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 oSerPheSerGluPhePheIleAsnMetGlyArgLeuPheThrLysVall 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 leGluLysValGlnAlaLeuProSerLysLysGlnArgIleGlnThrLeu 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 GlnSerAsnLeuIleAlaIleValArgCysPheTrpPheThrValGluSe 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448 GCCACA..........ATTTACTGGTTTACTGGAGTT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 rGlyLeuIleGluAsnHisGluGlyArgLysAlaTyrGlyAlaValLeuI 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 477 TGGGCTCTGCAAACANGGAGACTCCATAAAGGCATATGGTGCTGGGCTCC 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 leSerSerProGlnGluLeuGlyHisAlaPheIleAspAsnValArgVal 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 CAGCTITGCCCAGTTTTCCCAGGAAATTGGC......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakamachi 3327, Nara 631, Japan
Email: yoshidadews06, nara kindal.ac.jp
Dictyostellum discoideum cDNA project
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuProLeuGluLeuAspGln 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             577 CTCCCCCTGGAGCTGGAAG 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C93903.1 GI:3192312
                                                          erAspPheLeuAspHis.
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FEATURES
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121 121 9 239 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....SerIleProLeuTyrAsnGlnG 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAAAAAATTACCATTTAAT......CCATTTGA 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nThrSerThrProGlnGluThrLeuPheSerIleArg.HisPheAspGlu 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuValGluLeuThrSerLysLeuGluTrpMetLeuAspGlnGlyLeuLe 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....TTAGCTTCAATTGGTGCTTCTGATGAAGATATT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rValGluSerGlyLeuIleGluAsnHisGluGlyArgLysAlaTyrGlyA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTIGAATITGGATTATGTAAAGAAGGTGATACAATTAGGCCATATGGTG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276 laValLeulleSerSerProGlnGluLeuGlyHisAlaPheIleAspAsn 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 ValArgValLeuProLeuGluLeuAspGlnIleIleArgLeuProPheAs 309
                                                                                                                                                                                                                                                                                                                                                                                                                        176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 hrLysValileGluLysValGlnAlaLeuProSerLysLysGlnArgile 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 GlnThrLeuGlnSerAsnLeuIleAlaIleValArgCysPheTrpPheTh 259
                                                                                                                                                                                                                                                                                                                                                 243 GlnAlaValileLysPhePheGluLeuGluThrHisPheSerTyrTyrPr 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                            137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 rgTyrPheProIleAlaSerValMetArgThrLeuAspLysAspAsnPhe 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 GIGTATICCATGCAACTCAATATATAGACATCCATCCGTACCATTATAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 uLeuHisProSerPheSerGluPhePheIleAsnMetGlyArgLeuPheT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469 CGCATGCAATACTGAATATCCAATTACAACATTCCAACCACTTTACTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                             38 CAGGATATITCAAACTITITACAAGAATGIACIGGCTGGCGTATICGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                        159 oValSerGlyPheValAlaProHisGlnTyrLeuSerLeuLeuGlnAspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 SerLeuThrProAspLeuIleHisAspLeuLeuGlyHisValProTrpLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 ACACCAGAACCAGATTGTTGTCATGAATTATTAGGTCATGTTCCATTATT
                                                                                                                                                                                  Length: 221
Gaps: 5
Percent Identity: 27.602
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                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                207.50
1.687
55.656
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US-09-438-185-1047 x C93903
                                                                                                                                                                                                                                                                                                            seg 1/1 to: C93903
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                                                                                            ď
                                                                                                                                                                                    Quality:
Ratio:
                                                                                                                                                                                                                  Percent Similarity:
                                                                                            257
                                                                                                                                                                     alignment_scores
                                                                                          BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculose.

Mus musculuse.

Mus musculuse.

Mus musculuse.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukarmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases I to 596)

Marray.M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Marray.M., Hillier,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                            vm56612.rl Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1002262 5' similar to gb:J04758 Mouse tryptophan hydroxylase (MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston, R. William Mouse EST Project
The WashO-HMIN Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Faz: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 uLeuGlnAspArgTyrPheProIleAlaSerValMetArgThrLeuAspL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 GTTAGCCTTTCGAGTCTTTCACTGCACTATGTGAGACACAGTTCAG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 ysAspAsnPheSerLeuThrProAspLeuIleHisAspLeuLeuGlyHis 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 SerTyrTyrProValSerGlyPheValAlaProHisGlnTyrLeuSerLe 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Stratagene mouse Tcell 937311"
/tissue_type="Tcell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 4
Percent Identity: 34.839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
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/db_xref="taxon:10090"
/clone="IMAGE:1002262"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 447.
Location/Qualifiers
1. .596
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                                                                                                                                                                                                                                                                                                                                                                             AA596443
AA596443.1 GI:2411878
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59.355
                                                                            seq_name: gb_est9:AA596443
                                                                                                                                                                  seq_documentation_block:
LOCUS AA596443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:566478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
Percent Similarity:
619 TGAAATACTTG
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                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                        DEFINITION
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JOURNAL
COMMENT
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AUTHORS
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interest and

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c93147 Dictyostellum discoideum SS (H.Urushihara) Dictyostellum discoideum cDNA clone SSM681, mRNA sequence.
                        Gaps: 6
Percent Identity: 29.469
             Length:
           Ouality: 205.00
Ratio: 1.723
Percent Similarity: 57.488
lignment_scores
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sequence: 5'-CACGGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTACAGGCCGAGGCGCCGACATG-dT(30)BN-3' (Where B = A', C, or G and N = A', C, G, Or T). Average insert size 1.65' the figure of c-A' of the size of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANGECCGAGGGCONT, AVELAYS ANGLES INSERTS OF 10 N C G, Or T). AVELAYS CONTAINED INSERTS OF 10.5-4.0 kb). 15/15 colonies contained the solution of the solution o
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Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Bammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
| Chases 1 to 674)
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Unpublished (1999)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CLONE distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1863 row: g column: 05
Plate: LLCM1863 row: g column: 05
High quality sequence stop: 665.
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WIH-MGC http://mgc.nci.nih.gov/.
Wational Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 14-MAR-2001
clone IMAGE:4613404
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cloning as follows: 5' an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 LeuGlu.....serIleProLeuTyrAsnGl 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 495 ATAGCTTTAAAAAACCATTTTCAATTCGTTACAATCCATACACTCAATCA 544
                                                                                                                                                                                                      395 GACGCAIGCAAIACTGAAIAICCAAITACAACAITCCAACCACTITACIA 444
                                                                                                                                                                                                                                                                                                                      341
                                                                                                   309 AsnThrSerThrProGlnGluThrLeuPheSerIleArg.HisPheAspG 325
                                                                                                                                                                                                                                                                                                                                                                                                                          494
325 luLeuValGluLeuThrSerLysLeuGluTrpMetLeuAspGlnGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                445 TGTTGCAGAAAGTTTCCAAAAAGCAAAAGAACAAATGAGACAATTTGCTG
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Percent Identity: 29.348
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laptors were used in cloning as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG429401 674 bp mRNA 602499620F1 NIH MGC_75 Homo sapiens CDNA
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pcr. This library was
1 was constructed by Cl
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/db_xref="taxon:9606"
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Sfil (ggccgcctcggcc);
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                               366 AAGCAAAAAATTACCATTTAAT...
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1.897
58.152
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BG429401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 nGluLysTyrLeu 354
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
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KEYWORDS
SOURCE
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Washington ....

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Email: hargechorsh.cn
This clone is available at CHGC in Shanghai.
This clone is available at CHGC in Shanghai.

1. 658
1. 658
2. 670 mail: "Homo sapiens"

/ Ab_xref="taxon:9606"
/ Clone="ib="GLCGPII"
/ Clone=lib="GLCGPII"
/ Clone=lib="GLCGPII"
/ Lisue_type="corresponding non cancerous liver tissue"
/ Lisue_type="corresponding non cancerous liver tissue"
/ Lisue_type="corresponding"
/ Lisue
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Trl: 86-21-50801919(ex.45) Fax: 86-21-50801922 Exar: 86-21-50801922 Exar: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProLeuGluLeuAspGlnIleIleArgLeuProPheAsnThrSerThrPr 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 rPheSerGluPhePheIleAsnMetGlyArgLeuPheThrLysValIleG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 luLysValGlnAlaLeuProSerLysLysGlnArglleGlnThrLeuGln 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erSerProGlnGluLeuGlyHisAlaPheIleAspAsnValArgValLeu 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 CATCTTTGGTGATTACAGTACTGCTTATCAGAGAGCCAAAGCTTCTC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCTGGAGCTGGAGAAGACAGCCATCCAAAATTACACTGTCACGGAGTT 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 eValalaProHisGlnTyrLeuSerLeuLeuGlnAspArgTyrPheProI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 lealaSerValMetArgThrLeuAspLysAspAsnPheSerLeuThrPro 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 GCACACAGTACATCAAAGGATCCAAGCCCATGTATACCCCCGAACCT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 LysPhePheGluLeuGluThrHisPheSerTyrTyrProValSerGlyPh 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 ....crtgccrcrcrggggggcaccrgargaaracarrgaaagcrcgcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 GCTTTCCTCTCGGGATTTCTTGGGTGGCCTTGGCCTTCCGAGTCTTCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 CAGITICTGCAGACTIGCACTGGTTTCCGCCTCCGACCTGTAGCTGGCCT
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US-09-438-185-1047 x AV651521
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58.242
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408
                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Eukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

1 (bases 1 to 658)
(dian, B., Wu, T., Hung, Q., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H.

2 (a), Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Qu, J.,

2 eng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu

6., Yang, Y., Gu, W., Chen, Z., and Han, Z.

1 Homo sapiens cDNA clone

Unpublished (2000)

Contact: Zeguang Han

Contact: Zeguang Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block: 658 bp mRNA EST 07-SEP-2000 LACCUS AV651521 658 bp mRNA clone GLCCOF11 3', mRNA sequence. DEFITINITION AV651521 GLC Homo sapiens cDNA clone GLCCOF11 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eulleSerSerProGlnGluLeuGlyHisAlaPheIleAspAsnValArg 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCTGTCATCCTTTGGTGAATTACAGTACTGCTTATCAGAGAAGCCAAAG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 rThrProGlnGluThrLeuPheSerIleArgHisPheAspGluLeuValG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      489 GGAGTTCCAGCCCCTGTATTACGTGGCAGAGAGTTTTAATGATGCCAAGG 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValLeuProLeuGluLeuAspGlnIleIleArgLeuProPheAsnThrSe 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 sproserPheSerGluPhePheIleAsnMetGlyArgLeuPheThrLysV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 allleGluLysValGlnAlaLeuProSerLysLysGlnArglleGlnThr 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 TCCACTGCACACACACACATGGATCCAAGCCCATGTATACCCCC 186
                                                                                                                                                                                                                                                                                              161 rGlyPheValAlaProHisGlnTyrLeuSerLeuLeuGlnAspArgTyrP 178
                                                                                                                                                                                                                                                                                                                                                    87 TGCCTGCTTTCCTCTCTGGGTTTTCTTGGGTGGCCTTCCGAGTCT 136
                                                                                                                                                                                                                                                                                                                                                                                                                              178 heprollealaSerValMetArgThrLeuAspLysAspAsnPheSerLeu 194
                                                                                                                                                                  145 ValileLysPhePheGluLeuGluThrHisPheSerTyrTyrProValSe 161
                                                                                                                                                                                                                        37 GITTCICAGITCCIGCAGACIIGCACIGGITICCGCCICCGACCIGIAGC 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 Thr ProAspLeulleHisAspLeuLeuGlyHisValProTrpLeuLeuHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: BG429401 from: 1 to: 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV651521
AV651521.1 GI:9872535
                                      US-09-438-185-1047 x BG429401
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389 295

278

271

105

278 263 307

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

233

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164 ValAlaProHisGlnTyrLeuSerLeuLeuGlnAspArgTyrPheProIl 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est40:AV652188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uman.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
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                                                                                                                                                                                                                                                                                                                    305
                                                                                                                                                                                                                                                                                                                                                                                        263
                                                                                                                                               197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host-"DH10B (ampicillin resistant)"
//note-"Organ: Liver and Spleen; Vector: pr773D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Bco RI;
phis is a subtracted version of the original Soares fetal
liver spleen lwFLS library. 1st strand cDNA was primed
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 734)
                                                                                                                                                                                                                                                                              1 (bases 1 to 734)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                              A1056667 734 bp mRNA EST 29-SEP-1998 A1056667 734 bp mRNA corollogo 203666.x1 Soares_fetal_liver_spleen_inFLS_S1 Homo sapiens cDNA clone iMAGE:1674274 3' similar to gb:R03020 phenylalanine-4-HYDROXXLASE (HUMAN); mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   599 TTTCCACTTCTTGAAAGTACTGT.....576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 uAlaPheGlyLeuLeuSerAspPheLeuAspHis...GlnAlaValIleL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     575 .......GGCTTCCATGAAGATAACATTCCCCAGCTGGAAGACGTTCTC 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 ysphepheGluLeuGluThrHisPheSerTyrTyrProValSerGlyPhe 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 PheSerLeuTrpLysSerTyrCysProArgPhePheLeuAspTyrLeuGl 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dev_stage="20 week-post conception fetus"
lab_host="DH10B (ampicillin resistant)"
458 CCAGCCCTGTATTACGTGGCAGAGTTTTAATGATGCCAAGGAG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1 to: 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 189
Gaps: 4
Percent Identity: 29.630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer [5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1674274"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: AI056867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-438-185-1047 x AI056867/rev
                                                                                                                                                                         AI056867.1 GI:3330656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201.00
1.844
57.672
                                       seq_name: gb_est15:AI056867
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LOCUS A1056867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNT
                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                REFERENCE
FORTHORS
                                                                                                                                                                                                                                                                                                                                                      JOURNAL
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FEATURES

COMMENT

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 642)

Olian, B., Wu, T., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H., Xu, X., Li, N., Feng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Qu, J., Song, H., Cheng, Z., Qu, J., G., Yang, Y., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, F., Qu, J., Eu, G., Rang, Y., Gu, Y., Chen, Z. and Han, Z.

Homo sapiens CDNA clone
(Unpublished (2000)
Contact: Zequang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shouling Road, Zhangliang Hi-Tech Park, Pudong, Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                issue_type="corresponding non cancerous liver tissue" ev_stage="Adult"

        seq_documentation_block:
        642 bp
        mRNA
        EST
        07-SEP-2000

        LOCUS
        AV652188
        642 bp
        mRNA
        sequence.

        DEFINITION
        AV652188
        C. Homo sapiens cDNA clone GLCCXG04 3', mRNA sequence.

        ACCESSION
        AV652188
        GI:9873202

        VERSION
        AV652188:1
        GI:9873202

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 LeuileGluAsnHisGluGlyArgLysAlaTyrGlyAlaValLeuIleSe 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 ATCCTTTGGTGAATTCCAGTACTGCTTATCAGAGAAGCCTAAGCTTCTCC 131
                                                                                                                                                                                                                                                                                                                   306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 erAsnLeuIleAlaIleValArgCysPheTrpPheThrValGluSerGly 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 rSerProGlnGluLeuGlyHisAlaPheIleAspAsnValArgValLeuP 297
                                                                                                                                                                                                                                                                                                                                                                                                      214 PheSerGluPhePhelleAsnMetGlyArgLeuPheThrLysVallleGl 230
                                                                                                                                                                                                                                                                                                                                                                     230 uLysValGlnAlaLeuProSerLysLysGlnArglleGlnThrLeuGlnS 247
                                                           ealaSerValMetArgThrLeuAspLysAspAsnPheSerLeuThrProA 197
                                                                                                           432 CACACAGTACATCAGACATGGATCCAAGCCCATGTATACCCCCGGAACCTG 383
                                                                                                                                                                 213
                                                                                                                                                                                                                333
                                                                                                                                                                 spLeulleHisAspLeuLeuGlyHisValProTrpLeuLeuHisProSer
                                                                                                                                                                                              hanzg@chgc.sh.cn
one is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"./db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/clone_lib="GLC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50801919(ex.45)
                                                                                                                                                                                                                                                                                                          Tel: 86-21-50801919
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297 roLeuGluLeuAspGln 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 CCCTGGAGCTGGAGGAG 114
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Section 1

alignment\_scores

BASE COUNT ORIGIN

203

DEFINITION

ACCESSION

/dev.strage="10 week-post conception fetus"
//dev.strage="20 week-post conception fetus"
//lab\_host="DH10B (ampicillin resistant)"
//note="Organ: Liver and Spleen; Vector: pr/73D (Pharmacia)
with a modified polyllnker; Site\_1: Pac I: Site\_2: Eco RI;
with a subtracted version of the original Soares fetal
liver spleen lNFLS library. lst strand cDNA was primed
with a Pac I - oligo(dT) primer [5' Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 578)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kiraman, D., Kucaba, T., Lecy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., Washu-Nci human EST Project
Uppublished (1997) double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo." Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 374.
Location/Qualifiers /clone\_lib="Soares\_fetal\_liver\_spleen\_lNFLS\_S1" /sex="male" Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 524 ..ACATTCCCCAGCTTGGAAGAC.....GTTTCTCAG 495 494 TICCTGCAGACTIGCACTGGTTTCCGCCTCCGACCTGTAGCTGGCCTGCT 445 444 TICCICICGGGATITCTIGGGTGACCTGGCCTICCGAGICTICCACTGCA 395 131 luAlaPheGlyLeuLeuSerAspPheLeuAspH1sGlnAlaValIleLys 147 148 PhePheGluLeuGluThrHisPheSerTyrTyrProValSerGlyPheVa 164 lalaproHisGlnTyrLeuSerLeuLeuGlnAspArgTyrPheProIleA 181 1 others Length: 194 Gaps: 6 Percent Identity: 30.412

```
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

        seq_documentation_block:
        mRNA
        EST
        12-JAN-2001

        LOCUS
        BFP88142
        1050 bp
        mRNA
        seq-tolia cone IMAGE:4241484

        DEFINITION
        602113355F1
        MCLCSAP_Kid14
        Mus musculus cone IMAGE:4241484

        ACCESSION
        5', mRNA
        sequence.

        ACCESSION
        BF788142.1
        GI:12093178

by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Wote: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 AsnThrSerThrProGlnGluThrLeuPheSerIleArgHisPheAspGl 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410 ACTGTCACGGAGTTCCAGCCCTGTATTACGTGGCAGAGAGTTTTAATGA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 snValArgValLeuProLeuGluLeuAspGlnIleIleArgLeuProPhe 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 yAlaValLeuIleSerSerProGlnGluLeuGlyHisAlaPheIleAspA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 ThrValGluSerGlyLeulleGluAsnHisGluGlyArgLysAlaryrGl 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....ctrgccrcrcggrgcaccrgargarraca 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 leginThrLeuginSerAsnLeulleAlaileValArgCysPheTrpPhe 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 TIGAAAAGCICGCCACA.....ATTTACIGGITT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 eThrLysVallleGluLysValGlnAlaLeuProSerLysLysGlnArgI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 LeuLeuHisProSerPheSerGluPhePheIleAsnMetGlyArgLeuPh 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 TITICAGAICGCAGCTITGCCCAGTTTTCCCAGGAAATTGGC...... 199
                                                                                                                                                                                                                                                                                                                                                        159 ProvalSerGlyPheValAlaProHisGlnTyrLeuSerLeuLeuGlnAs 175
                                                                                                                                                                                                                                                                                                                                                                                                                                        175 pargTyrPheProlleAlaSerValMetArgThrLeuAspLysAspAsnP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 CCGAGTCTTCCACTGCACACAGTACATCAGACATGGATCCAAGCCCATGT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170
                                                                                                                                                                                               Gaps: 29.412
                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: BG569651 from: 1
                                                                                                                                                                                                                                                                     alignment_block:
US-09-438-185-1047 x BG569651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est92:BF788142
                                                                                                                                                                                     192.00
1.920
58.824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460 TGCCAAGGAG 469
                                                                                    143 a
                                                                                                                                                                                        Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                         alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200
                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       il (ggccgctcggcc); Site_2: Sfil (ggccattatggc); 5' and adaptors were used in cloning as follows: 5' adaptor quence: 5'-CACGGCATTATGGC-3' and 3' adaptor sequence: 5'-CACGGCGATTATGGC-3' adaptor sequence: 5'-CACGGCGATGATGGC-3' (where B = A, ATTCTAGGCGCGACGATGATGGT) Average insert size 1.85 or G and N = A, C, G, or T). Average insert size 1.85 (range 1.0-4.0 kb). 15/15 colonies contained inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note-"organ: llver; Vector: pDNR-LIB (Clontech); Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryofa, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 598)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNR Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortlum/LLML at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG569651 598 bp mRNA EST 10-APR-2001
602587352F1 NIH_MGC_76 Homo sapiens CDNA clone IMAGE:4715964 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tttp://mgc.nci.nih.gov/.
Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: Robert Strausberg, Ph.D.

Email: Concernent: CLONETERH Laboratories, Inc.

Tissue Procurement: CLONETERH Laboratories, Inc.

CON Library Preparation: CLONETECH Laboratories, Inc.

CON Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 GlnThrLeuGlnSerAsnLeulleAlaileValArgCysPherrpPheTh 259
                                                                                                                                                                                                                                                                                                                                                                                          TACTGGTTAC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                 J59 rValGluSerGlyLeuIleGluAsnHisGluGlyArgLysAlaTyrGlyA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 TGIGGAGITTGGGCTCTGCAAACAAGAGACTCCATAAAGGCATATGGTG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 laValLeulleSerSerProGlnGluLeuGlyHisAlaPhelleAspAsn 292
                                                                                                                                                                                                                                                                   226 hrlysvalileGluLysValGlnAlaLeuProSerLysLysGlnArgile 242
                                                                                                                                                                                   214 eSerGluPhe......phelleAsnMetGlyArgLeuPheT 226
                                                                                                                                                                                                                1::::::|||
294 TGCCCAGTTTCCCAGGAAATNTGCCTTGCCTCTCTGGGTGCACCT...G 248
                                           198 LeulleHisAspleuLeuGlyHisValProTrpLeuLeuHisProSerPh 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NIH_MGC_76"
/lab_host="DH10B (T1 phage-resistant)"
                                                                                                                                                                                                                                                                                                     247 ATGAATACATTGAAAAGCTCGCCACAATT.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://image.llnl.gov
plate: LLCM1563 row: h column: 13
High quality sequence stop: 598.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4715964"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 ValArgValLeuProLeuGluLeuAspGln 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 CCAAAGCTTCTCCCCTGGAGCTGGAGAAG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG569651.1 GI:13577304
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BG569651
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LOCUS
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seq_name: gb_est13:AA880857
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LOCUS AA880857
DEFINITION vx46f08.rl St
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ORIGIN
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JOURNAL
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AUTHORS
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 1050)

NH MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Londact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.in.gov

Tissue Procurement: Jeffrey E. Consortium (LINL)

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Library Preparation: Library Preparation: Library Preparation: Library Preparation: Libr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 IleHisAspLeuLeuGlyHisValProTrpLeuLeuHisProSerPhese 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rGluphePhelleAsnMetGlyArgLeuPheThrLysVallleGluLysV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 aProHisGlnTyriceuSerieuLeuGlnAspArgTyrPheProlleAlaS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 ervalMetArgThrLeuAspLysAspAsnPheSerLeuThrProAspLeu 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 rescargaacterregeacarereccerrettreagargerriec 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 ArgAsnLeuTrp.....TyrArgLeuLeuSerSerArgPheSerLe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 ulrpLysSerTyrCysProArgPhePheLeuAspTyrLeuGluAlaPhe. 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95. ACATGCCTGCTACGAGCACAACTTCCCTCTTCTGGAAAAGTACT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 AGGAAGACCIGGGGAACGGIGITCAGGACICTGGAAGGCCTIGIATAAAAC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 200
Gaps: 6
Percent Identity: 29.500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: BF788142 from: 1 to: 1050
                                                                                                                                                                                                                                                                                                                                                                                              plate: Liam9857 row: n column: 13
High quality sequence stop: 717.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-438-185-1047 x BF788142
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Ratio: 1.648
Percent Similarity: 57.500
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ORIGIN
                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 592) Maraa, Dietrich, N., Dubuque, T., Galsel, S., Kucaba, T., Lany, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Schellenberg, S., Steptoe, M., Tan, F., Underwood, K., Moore, B., Milson, R. and Dastocett, D., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                  AARBOBS7 592 bp mRNA EST 26-NAR-1998 vx46f08.rl Stratagene mouse lung 937302 Mus musculus CDNA clone IMAGE:1278279 5' similar to gb:R03020 PHENYLALANINE-4-HYDROXYLASE (HUMAN): gb:X51942 Mouse mRNA for phenylalanine hydroxylase (MOUSE AARBOBS7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mousest@watson.wustl.edu
Email: mousesest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Maria M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
44.44 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. :592.
Cyganism="Mus musculus"
Strain="C57BL/6 x CBA"
Adb_xref="taxon:10090"
Adone="IMAGE:1278279"
Adone="IMAGE:1278279"
Adone="Lib="stratagene mouse lung 937302"
                                                                                                                                                                   249 LeulleAlalleValArgCysPheTrpPheThrValGluSerGlyLeull 265
                                                                                                                232 alGlnAlaLeuProSerLysLysGlnArglleGlnThrLeuGlnSerAsn 248
                                282 ProGlnGluLeuGlyHisAlaPheIleAspAsnValArgValLeuPro 297
                                                                                                                                                                                                                                                                                  547 TTTGGAGAATTACAGTACTGTTTATCAGACAAAGCCAAAGCTCCTGCCC 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seg primer: -28ml3 revl ET from Amersham
High quality sequence stop: 430.
Location/Qualifiers
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Unpublished (1996)
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$56 PheTrpPheThrValGluSerGlyLeuIleGluAsnHisGluGlyArgLy 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 sAlaTyrGlyAlaValLeuIleSerSerProGlnGluLeuGlyHisAla. 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 ysGlnArgileGlnThrLeuGlnSerAsnLeuIleAlaIleValArgCys 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 ValprofrpLeuLeuHisProSerPheSerGluPhePheIleAsnMetGl 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 yArgLeuPheThrLysValIleGluLysValGlnAlaLeuProSerLysL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 SerTyrTyrProValSerGlyPheValAlaProHisGlnTyrLeuSerLe 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 uleuGlnAspArgTyrPheProlleAlaSerValMetArgThrLeuAspL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 ysaspasnPheSerLeuThrProAspLeuIleHisAspLeuLeuGlyHis 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 AGCCCATGTACACACCTGAACCTGATATCTGTCATGAACTCTTGGGACAT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 GIGCCTTGTTTCAGATAGAAGCTTTGCCCAGTTTTCTCAGGAAATTGG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....crrccarccrdcgcgccaccrd 377
                                                                                                                                                                                                                                                                                124 gPhePheLeuAspTyrLeuGluAlaPhe...GlyLeuLeuSerAspPheL 140
                                                                                                                                                                                                                                                                                                                                                                    40 euAspHis...GlnAlaValIleLysPhePheGluLeuGluThrHisPhe 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 TyrArgLeuLeuSerSerArgPheSerLeuTrpLysSerTyrCysProAr 124
                                                                                                                                                                                                                                                                                                              105 rcccccagcrccaagargritcrccagrritcrscagacrrcracrggriic 154
                                                                                                                                                                                                                              :::|||:::|||:::|||:::|||::::||
5 ITCAGAGTCCTGAACACCTTGTATAAAACACATGCCTGCTACGAGCACACAA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 PhelleAspAsnValArgValLeuProLeuGluLeuAspGln 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504 TITATCAGACAAGCCAAGNTCCTGCCCNTGGAGCTAGAGAAG 545
       Length: 198
Gaps: 6
Percent Identity: 29.293
                                                                                                                                                              to: 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378 ATGAGTACATTGAGAAACTGGCCACA...
                                                                                                                                                         Align seg 1/1 to: AA880857 from: 1
                                                                                                       alignment_block:
US-09-438-185-1047 x AA880857
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                                                   Percent Similarity:
alignment_scores
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